## Sequence Listing

<110> Prof. Dr. Flügge, Ulf-Ingo 120> DNA-Sequences, which code a glucose-translocator, Plasmids, Bacteria, Yeasts and Plants containing This Tranlocator 30> plastidic glucose transporters <140> 09/719,168 <141> <150> 5652952 <151> 1999-06-13 <160> 6 <170> PatentIn Ver. 2.1 <210> 1 <211> 1874 <212> DNA <213> Zea mays <220> <221> CDS <222> (2)..(1630) <220> <221> 3'UTR <222> (1631)..(1874) <400> 1 g gca cga gag atg atg cgc tgc gct gca acg ggc ggc ggg tgc gtc gct 49 Ala Arg Glu Met Met Arg Cys Ala Ala Thr Gly Gly Gly Cys Val Ala 97 teg tgg age gge gat egg aga ttg eeg geg gte aac eec tge age gtg Ser Trp Ser Gly Asp Arg Arg Leu Pro Ala Val Asn Pro Cys Ser Val cgg atg ccg acg ggc aac gat ggg tgg tgc gcc ggc ctg agg tcg cgg 145 Arg Met Pro Thr Gly Asn Asp Gly Trp Cys Ala Gly Leu Arg Ser Arg 35 193 gcg gcg gat ctc gcc ggc ctc gag atg gcc aac ctg cgc ggc gtc Ala Ala Asp Leu Ala Gly Leu Glu Met Ala Asn Leu Arg Gly Gly Val 50 241 ggg ggg ctc ttc cgc gcg agc ccg cgc tac ggg cgc ttg caa gcc acg Gly Gly Leu Phe Arg Ala Ser Pro Arg Tyr Gly Arg Leu Gln Ala Thr 65 gcg gca gtt gac cct gaa gat att cca ttg gag aag gtt caa gtt aaa 289 Ala Ala Val Asp Pro Glu Asp Ile Pro Leu Glu Lys Val Gln Val Lys 85 tcc tca gga cat gtt ctg cca tat gtt ggc gtt gct tgt ttg ggg gct 337 Ser Ser Gly His Val Leu Pro Tyr Val Gly Val Ala Cys Leu Gly Ala 100 att ctg ttt ggt tac cat ctt ggt gtg gtc aat ggc gca ctt gaa tat 385

•																
11	e Leu	Phe 115	Gly	Tyr	His	Leu	Gly 120	Val	Val	Asn	Gly	Ala 125	Leu	Glu	Tyr	
	c gcg u Ala 130	Lys														433
_	g gtt l Val 5	-			_	-		_								481
	t tct y Ser	_	_	_						_				_	_	529
_	a gtc a Val			_			_		_	_	_		_		_	577
	c cgc e Arg															625
_	c tca l Ser 210		_		_											673
_	a att u Ile 5	_						_						_		721
	a att y Ile															769
	c tgg a Trp															817
· · · · · · · · · · · · · · · · · · ·	g gct ı Ala	_		_	-		_		-	-		_				865
	g caa n Gln 290															913
	a aaa y Lys 5	_	_	-		_		_		-	_	_	_	_		961
	a agt n Ser															1009
_	t tac g Tyr			-		-	-		-	_	_		_		_	1057
	g ctt n Leu															1105

.

							gat Asp									1153
							atg Met									1201
				-		_	ata Ile		-				-		_	1249
							tcc Ser									1297
					-	_	gtt Val 440			_	_			_		1345
	_			_			gtt Val							_		1393
							aag Lys									1441
		-					att Ile		_			_	_	_		1489
							gtg Val									1537
_		_	_	_			gct Ala 520				_			_		1585
_			-			-	agg Arg			_	_	_	_	tga		1630
tgta	actt	tg d	ctagt	cato	gc to	gtggd	cgccq	g tti	tggt	tat	cga	gaato	gca a	accaa	agcgct	1690
caa	ccgaç	gca t	tcctt	ggad	cc to	ggaga	actct	tto	ctagt	ttc	atgt	agtt	ctt a	agaaa	ataagc	1750
gaad	eggea	aag a	agtad	ccaat	c tt	aggt	gact	tg	gtgtg	gggt	tgt	gtcto	gaa a	ataaq	gtgaat	1810
tgga	attgt	ag a	aattt	caga	aa at	aagt	gaat	t tg	gatte	gtag	aatt	tcaa	aaa a	aaaa	aaaaaa	1870
aaaa	a															1874

<210> 2 <211> 542 <212> PRT

<213> Zea mays

<400> 2

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- Arg Met Pro Thr Gly Asn Asp Gly Trp Cys Ala Gly Leu Arg Ser Arg .  $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$
- Ala Ala Asp Leu Ala Gly Leu Glu Met Ala Asp Leu Arg Gly Gly Val $50 \\ 60$
- Gly Gly Leu Phe Arg Ala Ser Pro Arg Tyr Gly Arg Leu Gln Ala Thr 65 70 75 80
- Ala Ala Val Asp Pro Glu Asp Ile Pro Leu Glu Lys Val Gln Val Lys 85 90 95
- Ser Ser Gly His Val Leu Pro Tyr Val Gly Val Ala Cys Leu Gly Ala 100 105 110
- Ile Leu Phe Gly Tyr His Leu Gly Val Val Asn Gly Ala Leu Glu Tyr 115 120 125
- Leu Ala Lys Asp Leu Gly Ile Ala Glu Asn Ala Val Leu Gln Gly Trp 130 135 140
- Val Val Ser Thr Ser Leu Ala Gly Ala Thr Leu Gly Ser Phe Thr Gly 145 150 155 160
- Gly Ser Leu Ala Asp Lys Phe Gly Arg Thr Arg Thr Phe Ile Leu Asp 165 170 175
- Ala Val Pro Leu Ala Leu Gly Ala Phe Leu Ser Ala Thr Ala Gln Asp 180 185 190
- Ile Arg Thr Met Ile Ile Gly Arg Leu Leu Ala Gly Ile Gly 195 200 205
- Val Ser Ser Ala Leu Val Pro Leu Tyr Ile Ser Glu Ile Ser Pro Thr 210 215 220
- Glu Ile Arg Gly Thr Leu Gly Thr Val Asn Gln Leu Phe Ile Cys Ile 225 230 235 240
- Gly Ile Leu Ala Ala Leu Leu Ala Gly Leu Pro Leu Ala Gly Asn Pro 245 250 255
- Ala Trp Trp Arg Thr Met Phe Gly Ile Ala Val Val Pro Ser Ile Leu 260 265 270
- Leu Ala Val Gly Met Ala Phe Ser Pro Glu Ser Pro Arg Trp Leu Phe 275 280 285
- Gln Gln Gly Lys Val Thr Gln Ala Glu Leu Ala Val Lys Arg Leu Tyr 290 295 300
- Gly Lys Glu Met Val Thr Glu Ile Met Phe Asp Leu Arg Ala Ser Gly. 305 310 315 320
- Gln Ser Ser Glu Ser Glu Ala Gly Trp Phe Asp Leu Phe Ser Lys 325 330 335
- Arg Tyr Trp Lys Val Val Ser Val Gly Ala Ala Leu Phe Leu Phe Gln 340 345 350

Gln Leu Ala Gly Ile Asn Ala Val Val Tyr Tyr Ser Thr Ser Val Phe Arg Ser Ala Gly Ile Ala Ser Asp Val Ala Ala Ser Ala Leu Val Gly 375 Ala Ala Asn Val Phe Gly Thr Met Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg Lys Ser Leu Leu Ile Thr Ser Phe Ser Gly Met Gly Ala 410 Ser Met Leu Leu Ala Leu Ser Phe Thr Trp Lys Ala Leu Ala Pro Tyr Ser Gly Thr Leu Ala Val Val Gly Thr Val Leu Tyr Val Leu Ser Phe Ala Leu Gly Ala Gly Pro Val Pro Ala Leu Leu Pro Glu Ile Phe Ala Ser Arg Ile Arg Ala Lys Ala Val Ala Leu Ser Leu Gly Met 470 His Trp Val Ser Asn Phe Phe Ile Gly Leu Tyr Phe Leu Ser Val Val 490 Ser Lys Phe Gly Ile Ser Asn Val Tyr Leu Gly Phe Ala Ser Val Cys Ala Leu Ala Val Leu Tyr Ile Ala Gly Asn Val Val Glu Thr Lys Gly 520 Arg Ser Leu Glu Glu Ile Glu Arg Glu Leu Ser Val Ala Glu <210> 3 <211> 1653 <212> DNA <213> Solanum tuberosum <220> <221> CDS <222> (1)..(1419) <220> <221> 3'UTR <222> (1420)..(1653) ggc cgc tgc aga tca cac aga gtt cga gct gct gga gag gat att gag 48 Gly Arg Cys Arg Ser His Arg Val Arg Ala Ala Gly Glu Asp Ile Glu 10 gat gca gca cct ctc aaa gtt caa ggc caa tca tct gga tca gta ctt 96 Asp Ala Ala Pro Leu Lys Val Gln Gly Gln Ser Ser Gly Ser Val Leu ccc tat gtg ggt gta gct tgt ctg gga gca att tta ttt gga tat cac 144

Pro Tyr Val Gly Val Ala Cys Leu Gly Ala Ile Leu Phe Gly Tyr His

cta Leu	ggg Gly 50	gtg Val	gtg Val	aat Asn	ggt Gly	gcc Ala 55	ctt Leu	gag Glu	tac Tyr	cta Leu	gct Ala 60	aag Lys	gat Asp	ctt Leu	gga Gly	192
att Ile 65	gcc Ala	gag Glu	aac Asn	act Thr	gtt Val 70	ata Ile	caa Gln	gga Gly	tgg Trp	att Ile 75	gtt Val	agc Ser	aca Thr	gtt Val	ctt Leu 80	240
_		_		_		tca Ser					-	_	-	-		288
						ttt Phe										336
						act Thr										384
gga Gly	cgc Arg 130	tta Leu	ctt Leu	act Thr	gga Gly	att Ile 135	ggc Gly	att Ile	ggc Gly	atc Ile	tca Ser 140	tct Ser	gct Ala	att Ile	gtg Val	432
cca Pro 145	ctt Leu	tac Tyr	ata Ile	tct Ser	gag Glu 150	atc Ile	tca Ser	ccc Pro	act Thr	gaa Glu 155	att Ile	cgc Arg	ggc Gly	aca Thr	ctg Leu 160	480
						ttc Phe										528
gtg Val	gtt Val	gga Gly	ttg Leu 180	cct Pro	ttg Leu	tct Ser	gga Gly	aat Asn 185	cct Pro	tcg Ser	tgg Trp	tgg Trp	aga Arg 190	aca Thr	atg Met	576
						cca Pro										624
						cgg Arg 215										672
gaa Glu 225	gct Ala	gag Glu	aca Thr	tct Ser	att Ile 230	aaa Lys	agg Arg	cta Leu	tat Tyr	ggt Gly 235	aaa Lys	gaa Glu	aaa Lys	gtt Val	gct Ala 240	720
						gaa Glu										768
gat Asp	gct Ala	GJ Å aaa	tgg Trp 260	ctt Leu	gat Asp	cta Leu	ttt Phe	agt Ser 265	agc Ser	cgt Arg	tat Tyr	agg Arg	aaa Lys 270	gtt Val	gtt Val	816
						ttc Phe										864
gct	gtt	gtc	tat	tat	tcc	act	gcc	gtg	ttc	cgg	agt	gct	gga	att	aca	912

Ala	Val 290	Val	Tyr	Tyr	Ser	Thr 295	Ala	Val	Phe	Arg	Ser 300	Ala	Gly	Ile	Thr	
	_	_	_	-	_	-	_	-		_	-		-	ttt Phe		960
	_		_			_	_	_					-	agt Ser 335		1008
-			-				_	_	_		-	_	_	ctt Leu		1056
_					_	-	_							ctg Leu	_	1104
														gct Ala		1152
			-					-			-		_	att Ile		1200
														aac Asn 415		1248
														atc Ile		1296
_			_			_			_		_	_	-	gtg Val		1344
				_				-				_		gag Glu		1392
	cgt Arg							tga	gtgo	gtaca	aac a	atgaa	acago	ct		1439
gaga	agtaa	att 1	tcaga	attco	cg co	catco	cagto	g ggt	ctt	gatt	ttga	aagaq	gat 1	tctc	cacatt	1499
ggga	agtto	cta 1	ttati	gcga	ag ac	ctgga	agtto	g cat	cact	tac	ccti	ttago	cta 1	tctct	ttgat	1559
ttt	cttgt	ac q	gtcg	gcato	ca to	gaato	catgo	g aad	catto	gtaa	aaa	catg	aa o	ctgtt	atgga	1619
agat	gato	ccg (	cgtai	gatt	g ag	gtati	tcaa	a aaa	aa							1653

<sup>&</sup>lt;210> 4

<400> 4

Gly Arg Cys Arg Ser His Arg Val Arg Ala Ala Gly Glu Asp Ile Glu

<sup>&</sup>lt;211> 472

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Solanum tuberosum

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Pro Tyr Val Gly Val Ala Cys Leu Gly Ala Ile Leu Phe Gly Tyr His 35 40 45

Leu Gly Val Val Asn Gly Ala Leu Glu Tyr Leu Ala Lys Asp Leu Gly 50 55 60

Ile Ala Glu Asn Thr Val Ile Gln Gly Trp Ile Val Ser Thr Val Leu 65 70 75 80

Ala Gly Ala Phe Val Gly Ser Phe Thr Gly Gly Val Leu Ala Asp Lys 85 90 95

Phe Gly Arg Thr Lys Thr Phe Ile Leu Asp Ala Ile Pro Leu Ser Val

Gly Ala Phe Leu Cys Thr Thr Ala Gln Ser Val Gln Ala Met Ile Ile 115 120 125

Gly Arg Leu Leu Thr Gly Ile Gly Ile Gly Ile Ser Ser Ala Ile Val 130 135 140

Pro Leu Tyr Ile Ser Glu Ile Ser Pro Thr Glu Ile Arg Gly Thr Leu 145 150 155 160

Gly Thr Val Asn Gln Leu Phe Ile Cys Ile Gly Ile Leu Val Ala Leu
165 170 175

Val Val Gly Leu Pro Leu Ser Gly Asn Pro Ser Trp Trp Arg Thr Met 180 185 190

Phe Gly Leu Ala Leu Ile Pro Ser Val Leu Leu Ala Ile Gly Met Ala 195 200 205

Phe Ser Pro Glu Ser Pro Arg Trp Leu Tyr Gln Gln Gly Arg Ile Ser 210 215 220

Glu Ala Glu Thr Ser Ile Lys Arg Leu Tyr Gly Lys Glu Lys Val Ala 225 230 235 240

Glu Val Met Gly Asp Leu Glu Ala Ser Ala Arg Gly Ser Ser Glu Pro  $245 \hspace{1cm} 250 \hspace{1cm} 255$ 

Asp Ala Gly Trp Leu Asp Leu Phe Ser Ser Arg Tyr Arg Lys Val Val 260 265 270

Ser Ile Gly Ala Ala Met Phe Leu Leu Gln Gln Leu Ala Gly Ile Asn 275 280 285

Ala Val Val Tyr Tyr Ser Thr Ala Val Phe Arg Ser Ala Gly Ile Thr 290 295 300

Ser Asp Val Ala Ala Ser Ala Leu Val Gly Ala Ala Asn Val Phe Gly 305 310 315 320

Thr Thr Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg Lys Ser Leu 325 330 335

Leu Leu Ile Ser Tyr Thr Gly Met Ala Ala Ser Met Met Leu Leu Ser

340 345 350

Leu Ser Phe Thr Trp Lys Val Leu Thr Pro Tyr Ser Gly Thr Leu Ala 360 Val Leu Gly Thr Val Leu Tyr Val Leu Ser Phe Ser Leu Gly Ala Gly 375 Pro Val Pro Ala Leu Leu Pro Glu Ile Phe Ala Ser Arg Ile Arg 395 Ala Lys Ala Val Ala Leu Ser Leu Gly Val His Trp Ile Met Asn Phe 405 410 Phe Ile Gly Leu Tyr Phe Leu Ser Ile Val Thr Lys Phe Gly Ile Ser 425 Thr Val Tyr Met Gly Phe Ala Leu Ser Cys Leu Val Ala Val Val Tyr 440 Ile Thr Gly Asn Val Val Glu Thr Lys Gly Arg Ser Leu Glu Glu Ile Glu Arg Glu Leu Ser Pro Ala Ile 470 <210> 5 <211> 1864 <212> DNA <213> Spinacia oleracea <220> <221> CDS <222> (61)..(1716) <220> <221> 5'UTR <222> (1)..(60) <220> <221> 3'UTR <222> (1717)..(1864) <400> 5 ggcacgaggc gatcgctgct taatcaattt caactttcgg tttagaaaaa gagggggaaa 60 atg cag gcg tca act ttt atg gtc aaa ggc aat ttg ggt ttt gaa gtt Met Gln Ala Ser Thr Phe Met Val Lys Gly Asn Leu Gly Phe Glu Val 1 cag aac cgt aga gtg gct ggg ctt gct ggg ttg aaa ggg tta agc tca 156 Gln Asn Arg Arg Val Ala Gly Leu Ala Gly Leu Lys Gly Leu Ser Ser atc cgt tcc aat aat cta agt ttt gtg aat gtt aat gac aat aat tat 204 Ile Arg Ser Asn Asn Leu Ser Phe Val Asn Val Asn Asp Asn Asn Tyr 35 40 aag tot aat ooc tgt aaa ttg agt tgt ggg too ott tog atg ggt got

Lys Ser Asn Pro Cys Lys Leu Ser Cys Gly Ser Leu Ser Met Gly Ala

55

50

					ttg Leu												300
		_		_	aag Lys 85	_		_	-				_		_	_	348
	_			-	aaa Lys							_			_	_	396
		-		-	gct Ala	_	_		-		_						444
			_		gga Gly	_		_					_		_		492
					gtt Val												540
				_	ggt Gly 165							_	_	_	_		588
					acc Thr												636
	-			-	gcc Ala		_			_	_		_	_			684
	-			-	ggc Gly								_		-	_	732
:					gag Glu		_			_		_		_			780
		-		_	ctt Leu 245			_						_	_	-	828
	_		Leu		tta Leu	_				_					_		876
					gtt Val												924
	Cys		_	_	cct Pro					_					_	-	972
					gta Val												1020

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305	310		315		320
		•	caa ggt tct : Gln Gly Ser : 330	_	•
Ala Gly Trp	-		cgc tac agg a Arg Tyr Arg		-
	-	-	caa atg gca ( Gln Met Ala (		•
	Tyr Ser Thr	-	cga agt gct ( Arg Ser Ala ( 380		
			gca tca aat o Ala Ser Asn ' 395		
			caa gga aga a Gln Gly Arg : 410		
Met Thr Ser			tca atg ttg : Ser Met Leu :		
-		_	tac tcg ggc a Tyr Ser Gly	_	-
	Val Leu Tyr	-	ttt tca ctt o Phe Ser Leu 0 460		
			ttc gca tcc a Phe Ala Ser i 475	-	-
			cat tgg gcg f His Trp Ala : 490		-
Ile Gly Leu			acc aag ttt o Thr Lys Phe o		
gtg tat ttg o Val Tyr Leu o 515			Val Leu Ala V		
gct ggt aac o Ala Gly Asn v 530	Val Val Glu	• • •	-		
ctt gct cta a Leu Ala Leu : 545			gaggat acagti	ttttc tgtttt	tttg 1746

atctatagag aattatgtta ataattcccg gatttaggag tttgatgcta gttttcatgc 1806

<210> 6

<211> 551

<212> PRT

<213> Spinacia oleracea

<400> 6

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Gln Asn Arg Arg Val Ala Gly Leu Ala Gly Leu Lys Gly Leu Ser Ser

Ile Arg Ser Asn Asn Leu Ser Phe Val Asn Val Asn Asp Asn Asn Tyr

Lys Ser Asn Pro Cys Lys Leu Ser Cys Gly Ser Leu Ser Met Gly Ala

Gly Phe Ala Arg Leu Gly Leu Asp His Val Met Lys Ser Ser Pro Lys

Tyr Arg Ser Val Lys Ala Gln Ala Ala Ser Gly Gly Asp Leu Glu Asp

Ala Thr Pro Val Lys Tyr Gln Gly Lys Ser Ser Ala Ser Val Leu Pro

Tyr Val Gly Val Ala Cys Leu Gly Ala Ile Leu Phe Gly Tyr His Leu

Gly Val Val Asn Gly Ala Leu Asp Tyr Leu Ser Ala Asp Leu Ala Ile 135

Ala Gly Asn Thr Val Leu Gln Gly Trp Val Val Ser Ile Leu Leu Ala

Gly Ala Thr Val Gly Ser Phe Thr Gly Gly Ser Leu Ala Asp Lys Phe

Gly Arg Thr Lys Thr Phe Gln Leu Asp Ala Ile Pro Leu Ala Ile Gly

Ala Tyr Leu Cys Ala Thr Ala Gln Asn Val Gln Ile Met Met Ile Gly 200

Arg Leu Cys Gly Ile Gly Ile Gly Ile Ser Ser Ala Leu Val Pro

Leu Tyr Ile Ser Glu Ile Ser Pro Thr Glu Ile Arg Gly Ala Leu Gly 230 235

Ser Val Asn Gln Leu Phe Ile Cys Ile Gly Ile Leu Ala Ala Leu Val

Ala Gly Leu Pro Leu Ala Gly Asn Pro Leu Trp Trp Arg Thr Met Phe 265

Gly Ile Ala Thr Val Pro Ser Val Leu Leu Ala Leu Gly Met Gly Phe 280

- Cys Pro Glu Ser Pro Arg Trp Leu Phe Gln Gln Gly Lys Ile Val Glu 290 295 300
- Ala Glu Lys Ala Val Ala Ala Leu Tyr Gly Lys Glu Arg Val Pro Glu 305 310 315 320
- Val Ile Asn Asp Leu Arg Ala Ser Val Gln Gly Ser Ser Glu Pro Glu 325 330 335
- Ala Gly Trp Phe Asp Leu Phe Ser Ser Arg Tyr Arg Lys Val Val Ser 340 345 350
- Val Gly Ala Ala Leu Phe Leu Phe Gln Gln Met Ala Gly Ile Asn Ala 355 360 365
- Val Val Tyr Tyr Ser Thr Ser Val Phe Arg Ser Ala Gly Ile Ala Ser 370 375 380
- Asp Val Ala Ala Ser Ala Leu Val Gly Ala Ser Asn Val Ile Gly Thr 385 390 395 400
- Ala Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg Lys Ser Leu Leu 405 410 415
- Met Thr Ser Phe Ser Gly Met Ala Ala Ser Met Leu Leu Leu Ser Leu 420 425 430
- Ser Phe Thr Trp Lys Ala Leu Ala Pro Tyr Ser Gly Thr Leu Ala Val 435 440 445
- Val Gly Thr Val Leu Tyr Val Leu Ser Phe Ser Leu Gly Ala Gly Pro 450 455 460
- Val Pro Ala Leu Leu Pro Glu Ile Phe Ala Ser Arg Ile Arg Ala 465 470 475 480
- Lys Ala Val Ala Leu Ser Leu Gly Met His Trp Ala Ser Asn Phe Val 485 490 495
- Ile Gly Leu Tyr Phe Leu Ser Val Val Thr Lys Phe Gly Ile Ser Lys 500 505 510
- Val Tyr Leu Gly Phe Ala Ser Val Cys Val Leu Ala Val Leu Tyr Ile 515 520 525
- Ala Gly Asn Val Val Glu Thr Lys Gly Arg Ser Leu Glu Glu Ile Glu 530 535 540

Leu Ala Leu Ser Pro Ala Val 545 550